

In the Specification

Kindly replace the paragraph beginning at page 1, line 5 with the following paragraph:

--Aspects of the invention may have been made using funding from National Institutes of Health grants MGH 2238: RO1 A149757-02 and R21 A14589801.

Accordingly, the Government ~~may have has~~ rights in the invention.--

Kindly replace the paragraphs beginning at page 10, line 7 and ending on page 10, line 16 with the following paragraphs:

-- Figs. 12 A to C provides the MS-Fit and MS-Tag search results of a component protein of about 84 and 86 kDa (SEQ ID NOS 9-45, 121, and 46-51, respectively in order of appearance).

Figs. 13 A and B provides the MS-Fit search results of a component protein of about 94 kDa (SEQ ID NOS 52 -72 respectively in order of appearance).

Figs. 14 A to C provides the MS-Fit and MS-Tag search results of a component protein of about 65 kDa (SEQ ID NOS 74-106, 121, and 107-118, respectively in order of appearance).

Figs. 15 A and B provides the sequence alignment of human HSP 90- β (SEQ ID NOS: 119) and mouse HSP protein 84 (SEQ ID NOS: 4).

Figs. 16 A and B provides the sequence alignment of HSP 84 (SEQ ID NOS 4) and HSP 86 (SEQ ID NOS 120), both from the mouse. --

Kindly replace the paragraph beginning at page 56, line 31 with the following paragraph:

-- 7.5% acrylamide gels were run according to the method of Laemmli, under denaturing conditions. EL4CM24 and fractions eluted by ion exchange chromatography

were prepared for SDS PAGE by boiling with Laemmli buffer and 5% β -mercaptoethanol for three minutes. Silver staining of gels was achieved using the Silver Stain Plus kit (Bio-Rad; Hercules, Calif.). Sequencing of protein bands from silver stained gels was completed at the Proteomics Mass Spectrometry Lab at University of Massachusetts Medical Center using standard technologies. Further information is readily available regarding mass spectrometry analysis, including MS-Fit and MS-Tag searching on the following website: <http://prospector.ucsf.edu/>. Briefly, MS-Fit is a "peptide mass fingerprinting tool" that analyzes mass spectrometry data and attempts to "fit" the data to a protein sequence. These protein sequences can be from any known sequence and commonly are from existing databases. MS-Tag searching follows a similar methodology but attempts to match the ionic nature of the protein sequences.--